

HJ

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/737,476B

DATE: 08/09/2001

TIME: 12:43:23

Input Set : A:\09737476.txt

Output Set: N:\CRF3\08092001\I737476B.raw

4 <110> APPLICANT: Leo G.J. FRENKEN
 5 Cornelis P.E. van der LOGT
 6 Vin-Mien TEH
 7 Martine E. VERHOEYEN
 8 Joy E. WILKINSON
 9 Stephen A. JOBLING

11 <120> TITLE OF INVENTION: Production of Antibodies
 13 <130> FILE REFERENCE: PNK/060113/0275850 - T7060C
 15 <140> CURRENT APPLICATION NUMBER: US 09/737,476B
 17 <141> CURRENT FILING DATE: 2000-12-18
 19 <150> PRIOR APPLICATION NUMBER: EP 99310188.0
 21 <151> PRIOR FILING DATE: 1999-12-17
 23 <160> NUMBER OF SEQ ID NOS: 67
 25 <170> SOFTWARE: MS Word
 27 <210> SEQ ID NO: 1
 29 <211> LENGTH: 440
 31 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence ✓
 35 <220> FEATURE:
 37 <223> OTHER INFORMATION: VHH with peptide linker ✓
 39 <220> FEATURE:
 41 <221> NAME/KEY: CDS
 43 <222> LOCATION: (1)..(417)
 45 <400> SEQUENCE: 1

47	cag	gtg	cag	ctg	cag	gag	tca	ggg	gga	gga	ttg	gtg	cag	gct	ggg	ggc	48
48	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
49	1				5				10				15				
51	tct	ctg	aga	ctc	tcc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	ggt	cat	96
52	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His	
53					20				25				30				
55	ggt	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt	144
56	Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg	
57					35				40			45					
59	gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggt	aaa	gag	aca	tgg	tat	aaa	192
60	Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys	
61					50				55			60					
63	gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	aag	act	240
64	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Thr	
65	65					70			75			80					
67	acg	gtt	tat	ctg	caa	atg	aac	agc	ctg	aaa	cct	gaa	gat	acg	gcc	gtt	288
68	Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	
69						85			90			95					
71	tat	tat	tgt	gcc	gct	cga	ccg	gtc	cgc	gtg	gat	gat	att	tcc	ctg	ccg	336
72	Tyr	Tyr	Cys	Ala	Ala	Arg	Pro	Val	Arg	Val	Asp	Asp	Ile	Ser	Leu	Pro	
73					100				105			110					
75	gtt	ggg	ttt	gac	tac	tgg	ggc	cag	ggg	acc	cag	gtc	acc	gtc	tcc	tca	384
76	Val	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	

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77	115	120	125	
79	gaa caa aaa ctc atc tca gaa gag gat ctg aat taataaggc taagctcgaa			437
80	Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn			
81	130	135		
83	ttc			440
86	<210> SEQ ID NO: 2			
88	<211> LENGTH: 139			
90	<212> TYPE: PRT			
92	<213> ORGANISM: Artificial Sequence ✓			
94	<220> FEATURE:			
96	<223> OTHER INFORMATION: VHH with peptide linker ✓			
98	<400> SEQUENCE: 2			
100	Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly			
101	1	5	10	15
103	Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His			
104	20	25	30	
106	Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg			
107	35	40	45	
109	Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys			
110	50	55	60	
112	Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr			
113	65	70	75	80
115	Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val			
116	85	90	95	
118	Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro			
119	100	105	110	
121	Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser			
122	115	120	125	
124	Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn ✓			
125	130	135		
128	<210> SEQ ID NO: 3			
130	<211> LENGTH: 11			
132	<212> TYPE: PRT			
134	<213> ORGANISM: Artificial Sequence ✓			
136	<220> FEATURE:			
138	<223> OTHER INFORMATION: myc linker ✓			
140	<400> SEQUENCE: 3			
142	Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn			
143	1	5	10	
146	<210> SEQ ID NO: 4			
148	<211> LENGTH: 471			
150	<212> TYPE: DNA			
152	<213> ORGANISM: Artificial Sequence ✓			
154	<220> FEATURE:			
156	<223> OTHER INFORMATION: VHH with linker ✓			
158	<220> FEATURE:			
160	<221> NAME/KEY: CDS			
162	<222> LOCATION: (1)..(459)			
164	<400> SEQUENCE: 4			

RAW SEQUENCE LISTING
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166	cag	gtg	cag	ctg	cag	cag	tca	ggg	gga	gac	ttg	gtg	cag	gct	ggg	ggg	48
167	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
168	1				5						10				15		
170	tct	ctg	aga	ctc	tcc	tgt	gta	gct	tct	gaa	agc	agc	ttc	agc	aac	aat	96
171	Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Glu	Ser	Ser	Phe	Ser	Asn	Asn	
172					20				25				30				
174	cac	atg	ggc	tgg	tac	cgc	cgg	gct	cca	ggg	aac	cag	cgc	gag	ctg	gtc	144
175	His	Met	Gly	Trp	Tyr	Arg	Arg	Ala	Pro	Gly	Asn	Gln	Arg	Glu	Leu	Val	
176		35				40						45					
178	gca	act	att	agt	cct	ggt	ggt	agc	aca	cac	tat	gta	gac	tcc	gtg	aag	192
179	Ala	Thr	Ile	Ser	Pro	Gly	Gly	Ser	Thr	His	Tyr	Val	Asp	Ser	Val	Lys	
180		50				55			60								
182	ggc	cga	tcc	acc	atc	tcc	cga	gac	aac	gcc	aag	aac	aca	gtg	tat	cta	240
183	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu	
184	65		70				75					80					
186	caa	atg	gac	agc	ctg	aaa	cca	gag	gac	acg	gcc	gtc	tat	tac	tgt	gct	288
187	Gln	Met	Asp	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
188					85			90			95						
190	gcc	aag	ggg	agg	ggg	ctg	cag	gct	atg	cag	tac	tgg	ggc	cag	ggg	acc	336
191	Ala	Lys	Gly	Arg	Gly	Leu	Gln	Ala	Met	Gln	Tyr	Trp	Gly	Gln	Gly	Thr	
192		100				105						110					
194	ctg	gtc	acc	gtc	tcc	tca	gcg	cac	cac	agc	gaa	gac	ccc	agc	tcc	gct	384
195	Leu	Val	Thr	Val	Ser	Ser	Ala	His	His	Ser	Glu	Asp	Pro	Ser	Ser	Ala	
196		115				120					125						
198	gcc	gcc	cat	cac	cat	cac	cac	ggg	gcc	gca	gaa	caa	aaa	ctc	atc	432	
199	Ala	Ala	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile		
200	130				135					140							
202	tca	gaa	gag	gat	ctg	aat	ggg	gcc	gca	tagtaacaat	tg					471	
203	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala								
204	145				150												
207	<210>	SEQ ID NO:	5														
209	<211>	LENGTH:	153														
211	<212>	TYPE:	PRT														
213	<213>	ORGANISM:	Artificial Sequence	✓													
215	<220>	FEATURE:															
217	<223>	OTHER INFORMATION:	VHH with linker	✓													
219	<400>	SEQUENCE:	5														
221	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
222	1				5				10			15					
224	Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Glu	Ser	Ser	Phe	Ser	Asn	Asn	
225					20				25			30					
227	His	Met	Gly	Trp	Tyr	Arg	Arg	Ala	Pro	Gly	Asn	Gln	Arg	Glu	Leu	Val	
228		35				40						45					
230	Ala	Thr	Ile	Ser	Pro	Gly	Gly	Ser	Thr	His	Tyr	Val	Asp	Ser	Val	Lys	
231	50					55				60							
233	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu	
234	65				70				75			80					
236	Gln	Met	Asp	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
237					85				90			95					

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239 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
240 100 105 110
242 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
243 115 120 125
245 Ala Ala His His His His Gly Ala Ala Glu Gln Lys Leu Ile
246 130 135 140
248 Ser Glu Glu Asp Leu Asn Gly Ala Ala
249 145 150
252 <210> SEQ ID NO: 6
254 <211> LENGTH: 468
256 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence ✓
260 <220> FEATURE:
262 <223> OTHER INFORMATION: VHH with linker ✓
264 <220> FEATURE:
266 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(456)
270 <400> SEQUENCE: 6
272 cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg 48
273 Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly
274 1 5 10 15
276 tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata 96
277 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
278 20 25 30
280 gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc 144
281 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
282 35 40 45
284 gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag 192
285 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
286 50 55 60
288 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg 240
289 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
290 65 70 75 80
292 caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct 288
293 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
294 85 90 95
296 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg 336
297 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
298 100 105 110
300 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc 384
301 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
302 115 120 125
304 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca 432
305 Ala His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
306 130 135 140
308 gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 468
309 Glu Glu Asp Leu Asn Gly Ala Ala ✓
310 145 150
313 <210> SEQ ID NO: 7

RAW SEQUENCE LISTING
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Input Set : A:\09737476.txt
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315 <211> LENGTH: 152
 317 <212> TYPE: PRT
 319 <213> ORGANISM: Artificial Sequence ✓
 321 <220> FEATURE:
 323 <223> OTHER INFORMATION: VHH with linker ✓
 325 <400> SEQUENCE: 7
 327 Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly
 328 1 5 10 15
 330 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
 331 20 25 30
 333 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
 334 35 40 45
 336 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
 337 50 55 60
 339 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
 340 65 70 75 80
 342 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 343 85 90 95
 345 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
 346 100 105 110
 348 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
 349 115 120 125
 351 Ala His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
 352 130 135 140
 354 Glu Glu Asp Leu Asn Gly Ala Ala
 355 145 150
 358 <210> SEQ ID NO: 8
 360 <211> LENGTH: 462
 362 <212> TYPE: DNA
 364 <213> ORGANISM: Artificial Sequence ✓
 366 <220> FEATURE:
 368 <223> OTHER INFORMATION: VHH with linker ✓
 370 <220> FEATURE:
 372 <221> NAME/KEY: CDS
 374 <222> LOCATION: (1)..(450)
 376 <400> SEQUENCE: 8
 378 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
 379 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
 380 1 5 10 15
 382 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
 383 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 384 20 25 30
 386 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
 387 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 388 35 40 45
 390 gag ttt gtc gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
 391 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 392 50 55 60
 394 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/737,476B

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Input Set : A:\09737476.txt

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